



SEQUENCE LISTING

<110> Bunn

<120> Compositions and Methods of Treating Diabetes

<130> 18989-032

<140> 10/772,076

<141> 2004-02-03

<150> 60/444,784

<151> 2003-02-03

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 1676

<212> DNA

<213> Homo sapiens

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<211> 487

<212> PRT

<213> Homo sapiens

<400> 2

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 Tyr Pro Thr Gly Leu Phe Thr Pro Glu Leu Asp Arg Leu Gln Ile Gly
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 Asp Phe Val Ser Val Ser Ser Pro Glu Gly Asn Phe Lys Ile Ser Lys
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 Phe Gln Glu Leu Glu Asp Leu Phe Leu Leu Ala Ala Gly Thr Gly Phe
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 Thr Pro Met Val Lys Ile Leu Asn Tyr Ala Leu Thr Asp Ile Pro Ser
 370 375 380
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 385 390 395 400
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 405 410 415
 Asp Val Glu Phe Val Leu Ser Ala Pro Ile Ser Glu Trp Asn Gly Lys
 420 425 430
 Gln Gly His Ile Ser Pro Ala Leu Leu Ser Glu Phe Leu Lys Arg Asn
 435 440 445
 Leu Asp Lys Ser Lys Val Leu Val Cys Ile Cys Gly Pro Val Pro Phe
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 <213> Homo sapiens

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 Ser Pro Tyr Met Glu Tyr His Pro Gly Gly Glu Asp Glu Leu Met Arg
 50 55 60

Ala Ala Gly Ser Asp Gly Thr Glu Leu Phe Asp Gln Val His Arg Trp
65 70 75 80

Val Asn Tyr Glu Ser Met Leu Lys Glu Cys Leu Val Gly Arg Met Ala
85 90 95

Ile Lys Pro Ala Val Leu Lys Asp Tyr Arg Glu Glu Glu Lys Lys Val
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<213> Homo sapiens

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Asp Ser Phe Arg Ala Glu Thr Ile Ile Lys Asp Cys Leu Tyr Leu Ile
35 40 45

His Ile Gly Leu Ser His Glu Val Gln Glu Asp Phe Ser Val Arg Val
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<213> Homo sapiens

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35 40 45

Gly Gln His Val Tyr Leu Lys Leu Pro Ile Thr Gly Thr Glu Ile Val
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 Lys Pro Tyr Thr Pro Val Ser Gly Ser Leu Leu Ser Glu Phe Lys Glu
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 Pro Val Leu Pro Asn Asn Lys Tyr Ile Tyr Phe Leu Ile Lys Ile Tyr
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 Pro Thr Gly Leu Phe Thr Pro Glu Leu Asp Arg Leu Gln Ile Gly Asp
 100 105 110
 Phe Val Ser Val Ser Ser Pro Glu Gly Asn Phe Lys Ile Ser Lys Phe
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 Gln Glu Leu Glu Asp Leu Phe Leu Leu Ala Ala Gly Thr Gly Phe Thr
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 Pro Met Val Lys Ile Leu Asn Tyr Ala Leu Thr Asp Ile Pro Ser Leu
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 Arg Lys Val Lys Leu Met Phe Phe Asn Lys Thr Glu Asp Asp Ile Ile
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 Trp Arg Ser Gln Leu Glu Lys Leu Ala Phe Lys Asp Lys Arg Leu Asp
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 Val Glu Phe Val Leu Ser Ala Pro Ile Ser Glu Trp Asn Gly Lys Gln
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 Gly His Ile Ser Pro Ala Leu Leu Ser Glu Phe Leu Lys Arg Asn Leu
 210 215 220
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 <213> Mus musculus

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 35 40 45

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 50 55 60
 Ala Ala Gly Ala Asp Gly Thr Asp Leu Phe Asn Glu Val His Arg Trp
 65 70 75 80
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 85 90 95
 Val Lys Pro Ala Val Pro Lys Asp Cys His Glu Gly Lys Arg Val Leu
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 Asn Gly Met Leu Pro Lys Ser Gln Met Ser Asp Thr Leu Pro Arg Asp
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 Lys Asn Ile Ser Leu Asp Ser Val Ile Val Asp Leu Gln Asp Asp Ser
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 Gly Leu Ser His Glu Val Gln Glu Asn Phe Ser Val Arg Val Ile Glu
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 210 215 220
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 225 230 235 240
 Lys Lys Asp Thr Gly Leu Tyr Tyr Arg Arg Cys Gln Leu Ile Ser Lys
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 Ser Leu Leu Ser Asp Phe Lys Glu Pro Val Leu Ser Pro Asn Lys Tyr
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 325 330 335
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 340 345 350

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 <213> Rattus norvegicus

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 35 40 45
 Ser Pro Tyr Met Glu Tyr His Pro Gly Gly Glu Asp Glu Leu Met Arg
 50 55 60
 Ala Ala Gly Ala Asp Gly Thr Asp Leu Phe Asn Glu Val His Arg Trp
 65 70 75 80
 Val Asn Tyr Glu Ser Met Leu Lys Glu Cys Leu Val Gly Arg Met Ala
 85 90 95
 Val Lys Pro Ala Val Pro Lys Asp Cys His Glu Gly Lys Arg Val Leu
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 Asn Gly Met Leu Pro Lys Ser Gln Val Thr Asp Thr Leu Pro Arg Glu

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Asp	His	Ser	Tyr	Leu	Ile	His	Ile	Gly	Leu	Ser	His	Glu	Val	Gln	Glu
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Asn	Phe	Ser	Val	Arg	Val	Ile	Glu	Asn	Val	Gly	Lys	Ile	Glu	Ile	Val
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210					215						220				
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225					230					235					240
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				245					250					255	
Leu	Phe	Cys	Leu	Met	Leu	Pro	Pro	Ser	Thr	His	Leu	Gln	Val	Pro	Val
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Phe	Val	Ser	Val	Ser	Gly	Pro	Glu	Gly	Asn	Phe	Lys	Val	Ser	Lys	Leu
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Pro	Met	Val	Thr	Val	Leu	Asn	His	Ala	Leu	Thr	His	Met	Ser	Ser	Leu
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Arg	Lys	Val	Lys	Leu	Met	Phe	Phe	Asn	Lys	Thr	Glu	Asp	Asp	Ile	Ile
385					390					395					400
Trp	Arg	Cys	Gln	Leu	Glu	Lys	Leu	Ala	Leu	Lys	Asp	Lys	Arg	Phe	His
				405					410					415	
Val	Glu	Tyr	Val	Leu	Ser	Ala	Pro	Ser	Pro	Glu	Trp	Asn	Gly	Lys	Gln

420 425 430
 Gly His Val Ser Arg Ala Leu Leu Ser Glu Phe Leu Gln Arg Ser Leu
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 Glu Asn Ser Lys Val Phe Leu Cys Ile Cys Gly Pro Thr Pro Phe Thr
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 Asp Glu Gly Ile Arg Leu Leu His Asp Leu Asn Phe Ser Asp Asp Glu
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<210> 8

<211> 495

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

<220>

<221> VARIANT

<222> (1)..(495)

<223> Wherein Xaa is any amino acid.

<400> 8

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 20 25 30

Lys Lys Xaa Asp Cys Trp Ile Cys Ile Arg Gly Phe Val Tyr Asn Val
 35 40 45

Ser Pro Tyr Met Glu Tyr His Pro Gly Gly Glu Asp Glu Leu Met Arg
 50 55 60

Ala Ala Gly Xaa Asp Gly Thr Xaa Leu Phe Xaa Xaa Val His Arg Trp
 65 70 75 80

Val Asn Tyr Glu Ser Met Leu Lys Glu Cys Leu Val Gly Arg Met Ala
 85 90 95

Xaa Lys Pro Ala Val Xaa Lys Asp Xaa Xaa Glu Xaa Xaa Lys Xaa Val
 100 105 110

Leu Asn Gly Met Leu Pro Lys Ser Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 115 120 125

Xaa Val Thr Asp Thr Leu Xaa Xaa Glu Gly Xaa Ser Xaa Pro Ser Tyr
 130 135 140

Asp	Trp	Phe	Gln	Thr	Xaa	Ser	Xaa	Val	Thr	Ile	Xaa	Xaa	Tyr	Thr	Lys	145	150	155	160
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Ser	Xaa	Arg	Ala	Glu	Xaa	Xaa	Ile	Lys	Asp	Xaa	Xaa	Tyr	Leu	Xaa	His	180	185	190	
Xaa	Gly	Leu	Ser	His	Glu	Val	Gln	Glu	Xaa	Phe	Ser	Val	Arg	Val	Xaa	195	200	205	
Glu	Xaa	Val	Gly	Lys	Ile	Glu	Ile	Val	Leu	Xaa	Lys	Lys	Glu	Xaa	Xaa	210	215	220	
Ser	Trp	Xaa	Xaa	Leu	Gly	Xaa	Xaa	Leu	Xaa	Xaa	His	Xaa	Ser	Xaa	Ile	225	230	235	240
Pro	Xaa	Lys	Asp	Thr	Gly	Leu	Tyr	Tyr	Arg	Xaa	Cys	Gln	Leu	Ile	Ser	245	250	255	
Lys	Glu	Asp	Val	Thr	His	Asp	Thr	Arg	Leu	Xaa	Cys	Leu	Met	Leu	Pro	260	265	270	
Pro	Ser	Thr	His	Leu	Gln	Val	Pro	Xaa	Gly	Gln	His	Val	Tyr	Leu	Lys	275	280	285	
Leu	Xaa	Xaa	Thr	Gly	Xaa	Glu	Ile	Val	Lys	Pro	Tyr	Thr	Pro	Val	Ser	290	295	300	
Xaa	Ser	Leu	Leu	Ser	Xaa	Phe	Lys	Glu	Pro	Val	Leu	Xaa	Xaa	Asn	Lys	305	310	315	320
Tyr	Ile	Tyr	Phe	Leu	Ile	Lys	Ile	Tyr	Pro	Xaa	Gly	Leu	Phe	Thr	Pro	325	330	335	
Glu	Leu	Asp	Arg	Leu	Gln	Ile	Gly	Asp	Phe	Xaa	Ser	Val	Ser	Xaa	Pro	340	345	350	
Glu	Gly	Asn	Phe	Lys	Xaa	Ser	Lys	Xaa	Gln	Glu	Xaa	Glu	Asp	Leu	Phe	355	360	365	
Leu	Leu	Ala	Ala	Gly	Thr	Gly	Phe	Thr	Pro	Met	Val	Xaa	Xaa	Leu	Asn	370	375	380	
Xaa	Ala	Leu	Xaa	Xaa	Xaa	Xaa	Ser	Leu	Arg	Lys	Val	Lys	Leu	Met	Phe	385	390	395	400
Phe	Asn	Lys	Thr	Glu	Asp	Asp	Ile	Ile	Trp	Arg	Xaa	Gln	Leu	Glu	Lys	405	410	415	
Leu	Ala	Xaa	Xaa	Xaa	Lys	Arg	Xaa	Xaa	Val	Glu	Xaa	Val	Leu	Ser	Ala	420	425	430	
Pro	Xaa	Xaa	Glu	Trp	Asn	Gly	Lys	Gln	Gly	His	Xaa	Ser	Xaa	Ala	Leu	435	440	445	

Leu Ser Glu Phe Leu Xaa Arg Xaa Xaa Xaa Xaa Ser Xaa Xaa Xaa Xaa
450 455 460

Cys Ile Cys Gly Pro Xaa Pro Phe Thr Xaa Xaa Gly Xaa Arg Leu Leu
465 470 475 480

His Asp Leu Asn Phe Ser Xaa Xaa Glu Ile His Xaa Phe Thr Ala
485 490 495

<210> 9
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence

<220>
<221> VARIANT
<222> (1)..(135)
<223> Wherein Xaa is any amino acid.

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Lys Gly Xaa Leu Ile Glu Val Thr Glu Glu Glu Leu Lys Lys His Asn
20 25 30

Lys Lys Xaa Asp Cys Trp Ile Cys Ile Arg Gly Phe Val Tyr Asn Val
35 40 45

Ser Pro Tyr Met Glu Tyr His Pro Gly Gly Glu Asp Glu Leu Met Arg
50 55 60

Ala Ala Gly Xaa Asp Gly Thr Xaa Leu Phe Xaa Xaa Val His Arg Trp
65 70 75 80

Val Asn Tyr Glu Ser Met Leu Lys Glu Cys Leu Val Gly Arg Met Ala
85 90 95

Xaa Lys Pro Ala Val Xaa Lys Asp Xaa Xaa Glu Xaa Xaa Lys Xaa Val
100 105 110

Leu Asn Gly Met Leu Pro Lys Ser Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125

Xaa Val Thr Asp Thr Leu Xaa
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<210> 10
<211> 105
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

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<221> VARIANT

<222> (1)..(105)

<223> Wherein Xaa is any amino acid.

<400> 10

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Xaa	Val	Thr	Ile	Xaa	Xaa	Tyr	Thr	Lys	Gln	Lys	Xaa	Ile	Xaa	Leu	Asp
			20					25					30		

Ser	Xaa	Ile	Val	Asp	Xaa	Gln	Xaa	Asp	Ser	Xaa	Arg	Ala	Glu	Xaa	Xaa
		35					40					45			

Ile	Lys	Asp	Xaa	Xaa	Tyr	Leu	Xaa	His	Xaa	Gly	Leu	Ser	His	Glu	Val
	50					55					60				

Gln	Glu	Xaa	Phe	Ser	Val	Arg	Val	Xaa	Glu	Xaa	Val	Gly	Lys	Ile	Glu
65					70				75					80	

Ile	Val	Leu	Xaa	Lys	Lys	Glu	Xaa	Xaa	Ser	Trp	Xaa	Xaa	Leu	Gly	Xaa
				85					90					95	

Xaa	Leu	Xaa	Xaa	His	Xaa	Ser	Xaa	Ile
		100						105

<210> 11

<211> 255

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
sequence

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<221> VARIANT

<222> (1)..(255)

<223> Wherein Xaa is any amino acid.

<400> 11

Pro	Xaa	Lys	Asp	Thr	Gly	Leu	Tyr	Tyr	Arg	Xaa	Cys	Gln	Leu	Ile	Ser
1				5					10					15	

Lys	Glu	Asp	Val	Thr	His	Asp	Thr	Arg	Leu	Xaa	Cys	Leu	Met	Leu	Pro
			20					25					30		

Pro	Ser	Thr	His	Leu	Gln	Val	Pro	Xaa	Gly	Gln	His	Val	Tyr	Leu	Lys
			35				40					45			

Leu	Xaa	Xaa	Thr	Gly	Xaa	Glu	Ile	Val	Lys	Pro	Tyr	Thr	Pro	Val	Ser	50	55	60	
Xaa	Ser	Leu	Leu	Ser	Xaa	Phe	Lys	Glu	Pro	Val	Leu	Xaa	Xaa	Asn	Lys	65	70	75	80
Tyr	Ile	Tyr	Phe	Leu	Ile	Lys	Ile	Tyr	Pro	Xaa	Gly	Leu	Phe	Thr	Pro	85	90	95	
Glu	Leu	Asp	Arg	Leu	Gln	Ile	Gly	Asp	Phe	Xaa	Ser	Val	Ser	Xaa	Pro	100	105	110	
Glu	Gly	Asn	Phe	Lys	Xaa	Ser	Lys	Xaa	Gln	Glu	Xaa	Glu	Asp	Leu	Phe	115	120	125	
Leu	Leu	Ala	Ala	Gly	Thr	Gly	Phe	Thr	Pro	Met	Val	Xaa	Xaa	Leu	Asn	130	135	140	
Xaa	Ala	Leu	Xaa	Xaa	Xaa	Xaa	Ser	Leu	Arg	Lys	Val	Lys	Leu	Met	Phe	145	150	155	160
Phe	Asn	Lys	Thr	Glu	Asp	Asp	Ile	Ile	Trp	Arg	Xaa	Gln	Leu	Glu	Lys	165	170	175	
Leu	Ala	Xaa	Xaa	Xaa	Lys	Arg	Xaa	Xaa	Val	Glu	Xaa	Val	Leu	Ser	Ala	180	185	190	
Pro	Xaa	Xaa	Glu	Trp	Asn	Gly	Lys	Gln	Gly	His	Xaa	Ser	Xaa	Ala	Leu	195	200	205	
Leu	Ser	Glu	Phe	Leu	Xaa	Arg	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Xaa	Xaa	210	215	220	
Cys	Ile	Cys	Gly	Pro	Xaa	Pro	Phe	Thr	Xaa	Xaa	Gly	Xaa	Arg	Leu	Leu	225	230	235	240
His	Asp	Leu	Asn	Phe	Ser	Xaa	Xaa	Glu	Ile	His	Xaa	Phe	Thr	Ala		245	250	255	